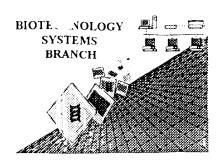
RAW SEQUENCE LISTING ERROR REPORT



0400 03-21-

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:	09/780,224
Source:	OIPE
Date Processed by STIC:	3/2/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,

2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address: http://www.uspto.gov/web/offices/pac/checker

SERIAL NUMBER: 09

ERROR DETECTED SUGGESTED CORRECTION

ATTN	: NEW RULES CASES: F	LEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE
	Wrapped Nucleics	The number/text at the end of each line "wrapped" down to the next line.
		This may occur if your file was retrieved in a word processor after creating it.
		Please adjust your right margin to .3, as this will prevent "wrapping".
2	Wrapped Aminos	The amino acid number/text at the end of each line "wrapped" down to the next line.
		This may occur if your file was retrieved in a word processor after creating it.
		Please adjust your right margin to .3, as this will prevent "wrapping".
3	Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.
4	Misaligned Amino Acid	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
	Numbering	between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
5	Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
		Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
6	Variable Length	Sequence(s) contain n's or Xaa's which represented more than one residue
	variable congili	As per the rules, each n or Xaa can only represent a single residue.
	-	Please present the maximum number of each residue having variable length and
		indicate in the (ix) feature section that some may be missing.
7	Patentin ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
· —	r dicitiii ver, 2:0 bog	sequence(s) Normally, Patentin would automatically generate this section from the
		previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
		to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
		sections for Artificial or Unknown sequences.
8	Skipped Sequences	Sequence(s) missing. If intentional, please use the following format for each skipped sequence
·	(OLD RULES)	(2) INFORMATION FOR SEQ ID NO:X:
	(OLD NOCCS)	(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
		(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
		This sequence is intentionally skipped
		This sequence is mentionally supplies
		Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
9	Skipped Sequences	Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
	(NEW RULES)	<210> sequence id number
	, ,	\$400> sequence id number
)		000
$_{10}J$	Use of n's or Xaa's	Use of n's and/or ≥ aa's have been detected in the Sequence Listing
	(NEW RULES)"	Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
	(,	In <220> to <223> section, please explain location of n or Xaa, and, which residue n or Xaa represents
11	Use of <213>Organism	Sequence(s) are missing this mandatory field or its response.
	(NEW RULES)	
		• • • • • • • • • • • • • • • • • • •
12	Use of <220>Feature	Sequence(s) are missing the <220>Feature and associated headings.
	(NEW RULES)	Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial" or "Unknown"
		Please explain source of genetic material in <220> to <223> section.
		(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
13	Patentin ver. 2.0 "bug"	Please do not use "Copy to Disk" function of Patentin version 2.0. This causes a corrupted
		file, Tesalting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
		Instead, please use "File Manager" or any other means to copy file to floppy disk.

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